OM nucleic - nucleic search, using sw model

Run on:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Perfect score:

Sequence:

Scoring table:

Searched:

us-09-596-194-59.rge

Gentore version 4.5 Copyright (c) 1993 - 2000 Compugen 1.td.	Result No.	Score	Query Match	Length	DB	ID	Description
		2537.8	93.0	2558		AF229053	
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			ryota;	Metazoa	; Cho	rdata; Craniata; Vertebr	Vertebrata: Enteleostomi.
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Gary,S.C., Zerillo,G.A., Gaw,J.U., Chiang-Moy,V. and Bockfield,S.
Direct Submission
Submitted (27-JAN-2000) Neurobiolody, Yale University, 313 Cedar
Submitted (27-JAN-2000)
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1 (bases I to 3476) Botstein,D.A., Goddard,A., Gurney,A.L., Smith,V., Watanabe,C.K. and Wood,W.!

Compositions and methods for the freatment of tumor Patent: WO 0075317-A 7 14-DEC-2000; Genentech, Inc. (US) [Accellon/Qualifiers

Homo sapiens Eukaryota, Motazoa, Chordata, Cianiata, Vertebruta, Entelvostoni, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

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17-JAN-2001

PAT

Sequence 7 from Patent W00075317, AX056675 AX056675.1 GI:102007

DEFINITION ACCESSION VERSION KEYWORDS SOURCE

AX056675

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Series: IRAK Plate: 19 Kow: n Column: 16
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer Irequency GRF
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Center code: BCM-HGSC
Web Site: https://www.lugsc.bcm.tmc.edu/cdnd/
Contact: villalon-bcm.tmc.edu.
Villalon, D.K., Luna R.A., Halle, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Hollowdy, M., Fellord, B, Hodyson, A., Bouck, J., Yu, W.,
Muzny,D.M., Glbbs,R.A.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (05-JUN-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                   2051 AGCAACTGGTGGTCCTGAGGTATCTGGGGTCCCTKGAGGAGAGAGGAGGAGAAGAA 2110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BC009117 3275 bp mkNA PRI 12-JHL-2001
Homo sapiens, chondroitin sultate protecolycan HEHAB/brevican,
clone MGC:18150 [MAGE:4154474, mRNA, complete cds.
HC009117
BC005117.1 GI:14318637
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: bavid N. Louis, M.D.
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/db_xret-"Locus1D:63827"
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Strausberg, R.
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TITLE
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/product."chondroitin sultate proteoglycan BEBAB/brevican" /protein_id-"AAH09117.1" /db_xref-"G1:14318638"

/LTABISTATIOD-"MAQUELPLIAALVIAQAPAALADVIEGISSEDRAFRVRIAGDAP LQGVLGGALT LPCHVHYLRPPPSRRAVIGSSRVKWIFI.SRRREARVLVARGYRKVNE AYRERVALPAYPASIJTDVSLALSELRPNDSGIYRCEVQHGIDDSSDAVEVKVKGVVFI. YREGSARVAFSFSGAQEACARIGAHIATPEQLYAAYIGGYEQCDAGWLSDQIVRYPIQ EATGGPELSUVPREESBETGSSEGAPELLPATRAPEGTRELFAPSFIDNSGRTAPAGTS
VQAQPVILPTDSASRGGVAVVPASGDCVPSPCHINGGTCLEBEEGYRCLCLPGYGGDLCD
VGAQPVILPTDSASRGGVAVVPASGDCVPSPCHINGGTCLEBEEGYRCLCLPGYGGDLCD
VGLRPCHPOMJARGGGVXCHFPSTRESMEBATTGCRMYGAHLASI STPEEGDFINNRYR
EYWHGINNRTI BGDFILMSDGVLIZ FUNNPOGPDSY FISGENCVVMWHDQGQMSDV
PCNYHISYTCKMGLYSCGPPPLELFIA AQVYCHRIRINYENTIVILRYRCKGLAGUNILPLI
MCQFRGKWBAPQI SCVPRRPARALHPREDPEGRGGRILGRWKALLIFPDSSPRHQF"

1 1016 c 1005 g 580 t IPPRIACYGDMDGI-PGVRNYGVVDPDDLYDVYCYAEDLNGFI-ĒLGDPPRKI TLEEAKAY CQERGAEIATTGQLYAANDGGLDHCSPGWLADGSVRYPI VYPSQRCGGGLPGVKYLJFI. PPNOTGFPRKISRENVYCEKDSAQPSA I PEASNPASNPASNGLEA I VTVTETLEELQI. PQEATESESRGA I YS I PIEMEDGGGSSTPEDPAEAPRI'LLEFET QSMVPPTGFSEEG KALEBEEKYFDEEEKFEFEEEFEEVEDBALWAWPSELSSPGPEASLPTEPAAVEKSLSG APARAVIQPGASDLPDGESFASRPPRVHGPPTFTLPTPKFRNLASPSPSTIVBAREVG

0; DB 9; Length 3275; Indels Score 2070.6; Pred. No. 0; 0; Mismatches 75.8%; Similarity 99.6 76; Conservative Query Match Best Logal S

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0 49 geagteteogregeagteteagetgeagetgeaggaetgaggetgeaeerygaggagg Caps cagnatygoccagotyttentgecectyntggcagecetggteetggeccaggeteetge 228 180 288 240 348 300 coactacctgroggccaccgccgggccgggctgtgctggctctccgcqqqgtcaagtg 408 360 468 528 480 540 09 588 648 600 708 cqvgggcgacgccactgcagggcgtgctcggcggcgcctcaccatcccttgccacqt ccaqcacqqcatrgatqacaqcagcgacqtqtggaggtcaagggtcaaagggqtcqtctt ggtgaacgaggcctaccggttccqcqtggcactgcctgcgtacccagcgtcgctcaccga qaelttechgteceggggeegggaggeagaggtgetggtagegeggggagtgega tetetacegagaggetetgecegetatgettteteettttetggggeeeagaggeetg tgcccgcattggagcccacatcgccaccccygagcaytctatgccgcctacttggggg Matches 2076; 69 121 289 303 349 409 469 421 529 481 589 541 649 601 500 ã ŝ 5 3 Š d δŏ qq ò g ò qq ò 9 δŽ g δy gg ò qq ŏ g ò

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ζŞ	769	Clatqagraalg galgclgqctgqctglcggaccqtgaggtalcccttcraaac 828
qn	721	CTATGRANGAAIGTGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
çy	829	Comacqagayyortyttacygaqacatgyatdgottoocyggytoogyaactatygtyt 888
qq	781	CCCACGAGAGGCGGGTFACGGAGACATGGATTCCCCCGGGGTCCGGAACTATCTTTTTTTT
δλ	88	99149acccqqalyacctclatgatqtqlactqttatgclyaaqacclaaalqqaqaact
qq	841	GGTGGACCCOGATGACCTCTATGATGTGTACTGTTATGCTGAAGACCTAAATGGAAACT
ογ	949	gttcctqgglyaccctccavaqaaqctgacattgqaygaaycacygycqtactgccayya
QQ	901	GTTCCTGGGTGACCCTCCAGAGAGCTGACATTGGAGGAAGCACGGGGGTACTGCTAGAGA
QY	1009	qcqqggtgraaqattgccaccacgqqccaactgtatgcagcctgggatggtqqcrtqqa
qq	961	GCGGGGTGCAGAGATGCCACCACGACCACCAACTGTATGCACCTGGGATGGTGGGCCAGA
δλ	1069	ocantycaycecaqqqlqqetaqetqqtqqqqtqtqtqtqtqtqcatacceatcqteaeaceaq
QQ	1021	CACTOTATE HELLELLE HELLE
ζŞ	1129	coagewrigt gytagagaet tarottagagaetototteetett oneraaeragae
qq	1081	CAGGGGTGTGGTGGGGGGGTTGGGTGTTTTTTTTTTTTT
δλ	1189	tgget tececaataageacageegetteaacy etaetgetteegagaeteggeereagee
qq	1141	TGGCTTCCCCAATAAGCACAGCGCTTCAACGICTACTGCTTCCGAGACTCGGCCCAACC
Qy	1249	ttctgcratcrctgaggcetccaacccagcctccaacccagcetctgatgactagage
QQ	1201	TTCTGCCATCCCTGAGGCCTCCAACCCAGCCTCCAACCCAGGCCTCTGATGGAGGC
QΥ	1309	tatogtcacaglyacagaqaccctygaggaactgcaggctgcctcaggaaqccacaqaga
qq	1261	TATCGICACAGIGACAGAGACCCIGGAGGAACIGCAGCTGCCTCAGGAAGCCACAGAGAG
Οy	1369	tgaateeegtggggeeatetactecateceatealggaggaeggaggagggaggete
qq	1321	TGAATCCCGTGGGGCCATCTACTCCATCCCATCATGGAGGAGGGAG
Οÿ	1429	nant ccagaaqacccagaagaccctagaactttyaaacacaal ccal
qq	1381	CACTICCAGAAGACCCAGCAGGGCCCTAGGACGCTCCTAGAATTTGAAGACAATCCAT
QY	1489	yataccgcccacgggqttctcagaagaggaanqtadggcattggaggaagaagaaata
QQ	1441	GGTACCGCCACGGGGTTCTCAGAAGGGAAGGTAGCATTGGAGAAGAAGAAATA
δλ	1549	Lgaaqatqaaqaaqaaqaqqaqqaqqaqqaqqaqqaqqaqqa
QQ	1501	501 TGAAGATGAAGAGAAAAAGGGGAAGAAGAAGAGAGGAGGA
δλ	1609	4. gagocatogrecagegateageageregggeet gaggeeteteeceeactgagee
QQ	1561	31GGGCATGGCCAGCGAGGTCAGCAGCGCGGGCCTGAGGCCTCTCCCCCAGTGAGCC
δý	1669	Agcagcagagagagagagactctcccaggcgccagcaagggcagtcctgcagcctggtgc
QQ	1621	NGCAGCCCAGGAGAAGTCACTCTCCCAGGCGCCAGCAAGAGCCAGTCTTTTTTTT
δy	1729	itcaccacticctgatggaggtcagagcttccaggcctccaagggtccatggaccacc
qq	1681	ATCACCACTTCCTGATGGGGGGGGGGGGGCTCCAGGCCTCCAAGGGTCCATGGACGACCAC

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Series: IRAK Plate: 12 Row: o Column: 3
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Web site: http://www.hgsc.bcm.tmc.edu/cdn:/
Context: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
Muzny,D.M., Gibbs,R.A.
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Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission Submitted (10-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
   /tissue_type="Brain, anaplastic oligodendroglioma with 1p/19q\ loss"
                                                                                                                                                                                                                                                                                                                                                                                                                                BC010571 3245 bp mKNA PRI 12-JUL-2001 Memo sapiens, chondroitin sulfate proteoglycan BEHAB/brevican, clone MGC:17338 IMAGE:4215184, mRNA, complete cds. BC010571.1 G1:14714840
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/db_xref-"LocusID:63827"
/db_xref-"taxon:9606"
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Email: cgapbs-r@mail.nih.gov
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COMMENT

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TPREAAYGDINGGE FOUNNY GVUDPDI LYDYYCY AEDLINGELFI GDPPEKI. I I LEEAKAY
COERGAET ATTGOLY AANDOGLIJHCSPGWI, AIGSVRYP I Y TPSGRCAGGI FOWT I FF
PROFIGEPRIKISTEN Y CFROSAQOSA I PEASNPASNPASNGALAI LYT BTLEELI, U
PORATESESRAR I YS I PI MEDGGGGSTPEDPARARTI, I FFETGSWPPT GFSEKEG
RALEEBEKYEDBEEKEEBEEEVEDBALWAMPSEL, SPRAEASLAFPRAAQEKSI, SO
APARAVIQPOASPI PINGEGERASBERVEDPRIKHI FFRENIASPSTI WEAREN)
                                                                            /db_xref="G1:14714841"
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VQAQPVLPTDSASRGGVAVVPASGDCVPSPCHNGGTGLEEERSVRCLCLFGPGGHLTD
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PCNYHLSYTCKMGLVSCGPPPELPLAQVFGRPRLRYBVLTVLRYRGRESIAQRNIALI
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/product="chondroitin sulfate proteoglycan BEHAB/brevican"
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AYRFRVALPAYPASLTDVSLALSELRPNDSG I YRCEVQHGI DDSSDAVEVKVKGVVFL
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FPNOTGFPNKHSKFRNYYCFRDSAQPSAIPEASNPASNPASDGLEALVIYTETLEELQL
PQEATESESRGAIYS IPIMEDGGGGSSTPEDPAEAPRTILEFETQSMVPPTGFSEEEG
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EATGGPELSGVPRGESEETGSSEGAPSLLPATRAPEGTRELEAPSEDNSGRTAPAGTS
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Soluble isoform, complete cds.
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human BEHAB/Drevican, a brain specific proteoglycan regulated
during cortical development and in qlioma
Gene 256 (1-2), 189-147 (2000)
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Buka;ota: Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi:
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 Chases 1 to 2878
Gary,S.C., Zerillo,C.A., Chiang,V.L., Gaw,J.U., Gray,G. and
Hockfield,S.
                                                                                1931 agetrewagugityreetleeetgetteeageracacaeggyeeetgagggtareaguga 1990
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gaggosactggtggtcctgagctatctggggtrcctcqaggagagagagugaugaugadaa 1930
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Gary.S.C., Zorillo.C.A., Gaw.J.U., Cheng-Moy.V. and Hockfield,S.
Direct Submission
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48. .2783
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/db_xref-"GI:10798901"
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0 617 7 37 922 daqqaaqcacqqqcqtactqccaqqaqcqqqtqcaqaqttqccaccacqqqccaactq 1042 937 ctggtqgcgcgqqqagtqcgcgtcaacggtgaacgaggcctaccggttccgcgtggcactg 502 562 622 682 14.5 805 862 982 202 262 322 382 257 442 317 377 437 497 557 677 797 857 137 197 Gaps 77 GYGCTGGGCTCYCCQCGGGTCAAGTGGACTTTCCTGTCCCGGGGCCCGGGAGGAGGTG 503 octgratacccagostcgctcaccgacgtriccctggcgctgagcgagctgrgcccaac gaggtmaaggtmaaagggqtmotttmtmtamagagggmtmtgcccgctatgctttc teettttetggggcecaggaggettgeecgeattggagveacategecaceeggag tteecegggggteegggaetatggtgtgtggaeeeeggatgaeetetatgatgtgtaetgt tatgetyaagaeetaaatgyagaaetgtteetgggtgaeeeteeagaggetgaeattg TATGCTGAAGACCTAAATGGAGAATTGTTCCTGGGTGACCCTCCAGAGAAGCTGACATTG acceaacceragecetgggtagectgeageatggeecaactgtteetgeecetgetggea 18 ACCCAACCCCAGCCCTGGGTAGCCTGCAGCATGGCCCAGCTGTTCCTGCCCCTGCTGGCA genetggteetggeeeraggeteetgeagetttageagatgttetggaaggagacagetea GCCCTGGTCCTGGCCCCAGGCTCCTGCAGCTTTAGCAGATGTTCTGGAAGGAGACAGCTCA gaggaccgrqcttttcgcytgcgcalegcgggcgacqcccartgcagggcgtgctcggc GAGGACCCCCTTTTCCCCTTCCCCGCCCACCCCCCCCACTCCAGGCCTTCCGC ggegeecteaceaterettgecaegtecaetaectgeggeeaeegeegageegeeggget gigetygggeteteegegggteaagtggaetiteetgteeegggggeegggaggeagagtg CTGGTGGGGGGGGGGGGGCGTCAAGGTGAACGAGGCCTACCGGTTCCGCGTGGCACTG gactcaggtatctategetgtgaggtecugeaeggeategatgaeageagegeegetgtg 498 GAGGICAAGGICAAAGGGGICGICITITCICIAACGAGAGGGGTICIGCCGGTATGCTITIC 558 TCCTTTTCTGGGGCCCAGGAGGCCTGTGCCCGCATTGGAGCCCACATCGCCACACCCCGGAG cagetetatgecgectacettgggggetatgaggeaatgtgatgetggetggetgteggat 803 rayacrytgaygtateecatecagaceecagagaggeetgttaeggagaratygatgye CAGACCGTGAGGTATCCCATCCAGACCCCACGAGGCCTGTTACGGAGACATGGC ó Length 2878; Indels 5 10; DB Pred. No. 0; 0; Mismatches Score 1975; 72.38; 99.58; Matches 1981; Conservative Similarity Query Match Local 623 863.1 738 BASE COUNT 683 743 923 983 143 78 563 879 263 138 323 198 383 258 443 3 qq á d qq ŏ 3 δŽ a ΟŸ 9 ô qqζŞ qq δ g ŏ ag ò a ŏ d à qq ò q 22 Š 5

1577 1882 2122 1497 1517 1757 1817 1043 tatycaycutgggatggtggcctggaccactgcagcccagggtggctayctgatggcagt 1102 1457 716 acteritectetreceaaceagactggetreceaataageacageeqetreaacque 1103 gigogolaceccalegicacacecagecagecigiggiggigggetic elegtificad 1283 aacccagcototgalggactagaggetalegteaeagtgacagagagacefagagauntg 1343 cagetyceteaqgaagecaraqaaytyaateerytygqqqecatetactericate gaggaggatggaggatgaggctctgtqqgcatggcccagcgagctcagcagccvqqqc entgaggeneteteteneaelgagecageceaggagagagteaeteteraggegeea aggenticeaagggticeatiggachanttantgagantergenanteragggaan ctgoccactgacagegecagecgagglagaglageegtgaleecogeateagglaatlet 918 TATGCAGCCTGGGATGGTGGCCTGGACCACTGCAGCCCAGGGTGGCTAGCTGATGGCAGT ACTICITACETTTCCCCAACCAGACTGGCTTCCCCAATAAGCACAGCGCGTTCAACGTC tactgot trogagactoggoccagnottotgreateertgaggectecaaereagentee atggaggacggaggaggtggaagntccantroagaaqaccagragaggcccntaggacg ctentagaattigaaanavaatonatgataneeqeeqqtteleaqaaqaqqaaqqt 1458 GAGGAGGAGGTGGAGGATGAGGCTCTGTGGGCATGGCCCAGCGAGGTTCAGCAGGCCGGGC 1638 AGGCCTCCAAGGGCCATGGACCACTACTGAGACTCTGCCCCACTCCCCAGGGAGAGGAAC 1823 ctagcalocccatcacettecacteriggttgaggcaagagagggggggggggggctggt ggtoctgagotatotqgggtcoctogaggagagagagagagagagagaggtcocqagggt gedecttedettedagecacacagggeeert gagggtacaggggaget ggaggeeee trigaagataatiriggaagaarigcoccagcaggarcicagigcaggccagig CTCCTAGAATTTTGAAACACAATCCATGGTACCCCCAAAGGGTTCTCTCAGAAGAGAAGT 1163 . 1038 1223 1403 1463 1338 1583 1643 1763 1698 1883 1943 1818 2003 2063 1938 qq qq g qq 8 q qq ã q ò g g ŏ q ά QQ õ g ò qq q g ò a ΩÝ g δ δ õ ŏ ŏ ă ò õ ŏ

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LQGVLGGALFIPCHVHYLRPSPSRRAAQGSPRVKWFFLSGGREAEVLVARGDRVKVSE
AYRFRVALPAYPASLTDVSLVLSELRPNDSGIYRCEVQHGIDDSSDAVEVKVKGVVFL
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SPPYKRAALQPGSSPPVDESELSHVADPTKTLPTPREGNLASPPSTLVGAREI
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DVGI.HFCSPGWDAFQGACYKHFSARRSWEEAENKCRMYGAIII.AS.I.STPEEQDFINNRY
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1026 c 991 q 618 t
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Molecular cloning of brevican, a novel brain proteoglycan of the
aggrecan/versican family
J. Biol. Chem. 269 (13), 10119-10126 (1994)
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/db_xref="taxon:9913"
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B.taurus Br.vican mRNA.
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JOURNAL REFERENCE AUTHORS TITLE	REF-RENCE AUTHORS TITLE TOIRNAL	DOLUMAL MEDILINE COMMENT FEATURES SOURC	misc_ CDS		siq_p mat_p misc_ repea	repea	MISC. BASE COUNT ORIGIN Query Mat Best 1002	Matches Oy 149 of Db 86 OY 209 o
1297 tggactagagqctatcgtcacagtqacagagaccttgqaqgaactqcagctgqctcagqa	1417 aggtagaagetecact.craqaagacccageaggeeeeetagaacttga 146	159 153 165 159	coccactgaurcagragaccayuagaagtcactricocaggogocagcaagggaagi 171 	1774 qqtrcatqqqactctqccrattccraqqqaqaqqacttqcccc	1954 gcttceagceacaeggqccccttgaggqtaccagggggcccctctgaagataa	2074 cagogocagoogaggtggagtggcoptggtccoopcatcaggtaattctgcocaaggctc 2133 	RESULT 7 RNRNABGPI LOCUS RNRNARGPI 2534 bp mkNA ROD 14-AUG-1996 DEFINITION R.HORVEGICUS mRNA for brevican, GPI-anchored isoform. ACCESSION X86406 VERSION X86406.1 GI:1491757 VERWORDS brevican; GPI-anchored protein; isoform. GREWORDS NORWAY rat. ORCANTRA Battale protecting isoform.	
QY OY 10b	oy oy oy	2 c p o	2 6 2 C	ab cy cy	oga oga	Oy Db	REST LOCU DEFI ACCE VERS KEYN SOUR	REFE AU TI

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Direct Submission
Submitted (18 APR-1995) E.D. Gundelfinger, Institute for
Submitted (18 APR-1995) E.D. Gundelfinger, Institute for
39008 Magdeburg, FKG
37 (bases 1 to 2534)
Seidenbecher, C.I., Richter, K., Rauch, U., Fassler, K., Garner, C.C.
and Gundelfinger, E.D.
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RGVLGGALAIPCHYHHIRPPPSRRAAPGFPRWKWTFLSGDREUFULVAKGLKVKWNFA
YRFRVALPAYPASLTDVSLVLSFLRPNINSGVYRCEVQHGTIDSSDAVEVKUKGVVFLY
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/protein_id="GAA60160.1"
/db_xref="G1:1491758"
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/note-"Ed anchor attachment signal"
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/ Organism-"Rattus norvegicus"
/ Strain-"Sprgue bavley"
/ db_xref-"taxon:10116"
/ tissue_type-"brain"
/ clone_lib-"lambda qt10"
/ clone_lib-"lambda gt11"

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    /bound_moiety-"hyalutonic acid"

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\circ	328	388		508	568	628 562	688	748		868	928	988		10		2	∞ ←	34
6 GICCHGACCCAAGCCCTGCAGCCCTCGCTGATGACC	9 egetitiogegiacognategeggosacycactarayayacytetegyeygaegae 	9 ctcarcattgccacgt.cactarctgcgccaccgccgaccgccggctgtqctg	9 ggctctccqcgggtcaagtgqacttrctgtcccgggggcggaggcagagggtcggtg 	9 grgrggggagtgcgcgtcaaggtgaacgaggcctaccggttccgcgtggcactgcctgc	9 Tacccagegtegeteacgaegtetectggegetgagegagetggeecaaegaetea 	9 getatctatcgctgtgaggtccagcacgcatcgatgacagcagcgacgctgtggaggtc 	9 aaggteaaagggfegtettetetaeegagggetetgeeggtatgetteteette 	9 letggggeepagaggettgtgreegettggaeceaategeeaecegageagete	9 fatgoogectacettgggggetalgagraalgtgatgetggetgteggateagaee	9 gtgaggtatrccatccagacccargagagcttacggagacatggattcccc (9 gggdtccggaactatggtgtggtggacccggatgaccttatgatgtgtartgttatgct	gaagacctaaatggagaactgttcctgggtgaccttcagagaagctgacattgaagaa 	geacygycytactgccagyaccygytqnagagattgccacccygyccaactgtatqca 	9cctgggatggtgcctggaccactgcagccraggtggctagctgatggcagtgtgcgc 	taccecategteacacecagecegegetgtggggggettgeetggtgteaagaetete :	ttoctettececaaceagaetggettececaataageacageetteaacgtetactge.	ttecgagacteggeettetgenateentgaggeeteeaaceageetenaaeena : 	gectetgatggaetagaggetategteacagtgaeagagaeeetggaggaaetgeagetg
4 4		32,	38 38	38	509		629 56.2	623	749	809	869	929	989	1049 983	1109	1169	1229	1289
<u> </u>	à a	Q Q	QY DD	Š Š	qa Ab	çy Db	QY Dp	QY Db	90 5	02 C.Y	93 Dp	QY Db	9.y Db	Qy Db	0.7 Dp	Qy Db	Q.Y Db	Qy

retedygaayeeacagaqaytgaateeegtyyygeealefacteeatereeteatygay 1408 gaatttgaaacacaatccatggtaccgccacgggggttctcagaagaggaaggtaaggca 1528 1451 CTGGAGGAAGAAGAAGAF-----TCAAAGACACAGAGACTCCGAAGGAA 1495 geotototococacigagocagoccaggagagagicacicicocaggogoratorada 1708 1829 tecesateaeettesartetggttgaggvaaggaggtggggggggggaetggtggleet 1888 1889 gagetaletquygleeetegaqqaqaqaqqqqqqqqq---aaqeteeqquqqqqqq | HITH | HITHIT | HITTIT | HITHIT | HIT 2158 GCGCCCAGTTCTCFGATCCTCTGCTCCCGGCCC----TACCGCTGACCCCCACCA 2210 2111 TCCCTCTCTGTCTCTCCTGTGGATCT------TTCTTCCATTCTGTCGTT 2157 gaggtygaaggatetgtgtggggeatggeeegageteageeageeequageeerqqqeeettaa 1556 GGGTTGGAAACAGAGCACTCACTCCCAGGTGTCCCCCA-------CCAGGGCAG gcaytect gradectyatigcateaecaet teet gal ggagagteagagget treagneet Coadqquecauqqacoacctactgaqactetqccactereaqqqqqqqqqqqqqqq 1946 cotterrightineayceacaegggeeetigagggtaneaqggagetqaaggeerint Creat garanty cogocy aggregation of the transfer of the transf 2051 CUGTGGGCGGCGTCTTTAATCCACCTCTCCCGGACCCTCTGGCCTTTGCCTCTAT acctgacetgtagtectttaaeecaeeteateeeaaaeteteetgteetttgeetteat 2243 telettanceacetelacelatgggleteceaaleleggalateceacellylggglatele 2303 ageteleogeglettlaceelgtgaleecageeceqeeactgaccatetglgaccellee 1349 1271 1409 1331 1469 1529 1589 1496 1649 1709 1769 1703 2066 2183 OD. ò qq ŏ qq ŏ qq $\overset{\circ}{\sim}$ Db δ QQ ò qq Q_{γ} qq qq ΟŽ δy Ω qq QΥ q δŽ ò qq ò g Q_{y} qq 3 Qγ qq ŏ

ô 9 ŏ 135 Š 5 ò 5 Š 9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 161318)
2423 octobecaaqqqteeteatr--aertattgeaqretteagqqteteggeetatttleeari 2480
                     248] actecetteateegeetytytyeegteeetttagetyeettetattgateteaggaag 2540
                                                                                                                               2541 cotgggagtocetteteaceenteaanetenggagteeaggagagaecegtaceneacag 2600
                                                                                                                                                                                                                                   2391 CCTGAGAGACCATCCCTGCCCCCTC-ACCTCTGGGGACCAGAATA----GTCACCCCAAAG 2445
                                                                                                                                                                                                                                                                                                            ayccttaaqraactacttctytygaaqtattttttgactgttt.atggaaaacaagccttq 2660
                                                                                                                                                                                                                                                                                                                                     2446 AGCCTTAAGCCACTACTGTGAAGTATTTTTTGACTGTTT.ATGAAAAAAAACAAGCCTTG 2505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (03-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humqueryssanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 8, 2001 this sequence version replaced gi:13990633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA HTG 04-MAY-2001
clone RP11-66D17, *** SEQUENCING IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: XGAP4; version 4.5
Chemistry: Dyo-terminator Big Dyo: 100% of reads
Consensus quality: 159757 bases at least 040
Consensus quality: 159820 bases at least 020
Consensus quality: 159820 bases at least 020
Insert size: 160318; sun-of-contigs
Insert size: 149188: 13.8% error; agarose-fp
Quality coverage: 9.28x in 020 bases; sum-of-contigs quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25476 25575: gap of 100 bp 25576 41767: contig of 16192 bp in length 41768 41867: gap of 100 bp 100 bp 41768 41868 44284: contig of 2417 bp in length 44285 44384: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALS90666.6 GI:13992142
HTG; HTGS_PHASE1; HTGS_FULLTOP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coverage: 9.97x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: SC
Web sile: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens chromosome 1 clone RP
PROGRESS ***, 11 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                         gaaataaatctctattaaaccgctttgta 2689
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2506 GAAATAAATCTGTATTAAACTGCTTTGTA 2534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: bA56D17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
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Direct Submission
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KEYWORDS
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COMMENT

RESULT.

LOCUS

SOURCE

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1465 octagaatt.Ugaaacacaatccatggtaccgcccacgggqttctcagaagaggaaggtaa 1524
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44385 54678: contig of 10294 bp in length 54679 54778: gap of 100 hp 54779 63296: contig of 8518 bp in length 63297 63396: gap of 100 hp 63397 77898: contig of 14502 bp in length.
                                                                                                         161318: contig of 60111 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1003 others
                                                                                                                                                                         96631: contig of 2578 bp in length
                                                                                                                                                                                      96532 96731: gap of 100 bp 96732 101107; contig of 4376 bp in length
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Pred. No. 2.5e-231;
0; Mismatches 1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              25576. 41767

//octe-assembly_rragment:02053

/rocte-"assembly_rragment:02053

/note-"assembly_rragment:02777

/ragment_chain:1"

//octe-"assembly_rragment:02777

/ragment_chain:1"
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fragment_chain:1"

101208. ...161208. ...161208

/note-"assembly_tragment:01356

fragment_chain:1"

a 40929 c 41273 g 40430 t 10
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fragment_chain:1"
77999. .81999
/note="assembly_tragment:03976
fragment_chain:1"
82100. .93953
                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_tragment:04075
fragment_chain:1
clone_end:8P6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54779. .63296
/note-"assembly_iraqment:01042
fraqment_chain:1"
63397. .7898
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94054. .96631
/note-massembly_tragment:02368
fragment_chain:1"
96732. .101107
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                                                                                                                                                                                                                                100 bp
                                                                                           100 bp
                                                                                                                                                                                                                                                                                                /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/chromosome-"1"
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                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                /clone-"kPl1-66D17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     vector_side:left"
25576. .41767
                                                                                                                                                                                                                   101108 101207; dap of 101208 161318. cont.
                                                                                                                                        82100 93953; cont
93954 94053; qap of
                                                                    63397 77898: cont
77899 77998: qap of
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82000 82099; dap of
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Best Local Similarity 99.99
Matches 1229, Conservative
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के व	1645 t	yaggecteteceerantgagecagnageceaggagagteacteteceaggogecaue 1704 	
Qy	1705 6	aagggcagtectgcagretgqtgcatcaccaettectgatggagagteagagettecag 1764 	
QY	1765 q 1 1162 d	geotecaaggticcatggaecacetactgagaetetgeceaeteceaggaaggaacet 1824 	
90 60	1825 8	18	
çy Db	1885 t	iggaageteegaqqqtge 19. 	
Qy	1945 c	cete 20 CCTC 14	
QY Db	2005 t	gaagataattetggaagaaetgeeeeageaggaeeteagtgeaggeeeagtget 2064 	
Qy Epp	2065 9 1462 G	cccartgacagogroagocagatgaattqorqtggtoroogoatoaggtaattotgc 21 	
Oy Dp	2125 co 1522 Cd	caaggetcaartgreetetetateeteettettetteeeetgeagetetgggteae 21) 	
90 70	2185 c 1582 C	Udacciglagicctitaacccaccatcatcccaactcictgicctitacritcatic 22.	
QY	2245 to 1642 To	CLtacceact.ctacctatgggtctccaatctcggatatccaccttgtqggtatctcag 23 	
67	2305 c	tigateccagecegocartga.catetgtgacert.cect 23.	
λ δ	2365 g	ccaltgggccrtccacctgtggctcacatctcgccagcccaragaqcatcctcaggcc 24	
Qý	2425 to 	ticcaagggloctcatcacctattgcagcctlcagggctcggcctattttcractactc 24	
Qy Db	2485 CC 11882 CC	ttcatcagcctgfgtgccqtcccctttagctgcctcctattgatctcagggaagctg 25	
Q 10p	2545 g	gaticeliticaececteaareteeggateeaggayaaceegtaeeegagee 2604 	
Qy Dp	2605 t	taagcaactacttctgtgaagtatttttgactgtttcatggaaaacaagccttggaaa 2664 	
δŽ	2665 ta		

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Assembly program: AAP4; version 4.5
Sequenting vector: plasmid: L09722; 100% or reads
Sequenting vector: plasmid: L09722; 100% or reads
Chemistry: Dye-terminator ET-amersham; 13% of reads
Chemistry: Dye-terminator ET-amersham; 13% of reads
Consensus quality: 174554 bases at least Q40
Consensus quality: 17589 bases at least Q40
Consensus quality: 17589 bases at least Q30
Consensus quality: 175840 bases at least Q30
Insert size: 17453; sum-of-configs
Insert size: 189736; 15% etzor; agarose-fp
Quality coverage: 6.84x in Q20 bases; sum-of-configs
Coverage: 6.57x in Q20 bases; sum-of-configs
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryola: Metazoa: Chordata, Craniata; Vertebrata: Euteleostomi;
Mammalia: Eutheria: Primates: Catarrhini; Bominidae; Homo.
] (buses 1 to 178753)
McJay.K.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (14 MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk
On M.r 20, 2001 this sequence version replaced gi:13473967.
                                                                                                                                                                  AL365181 178753 bp DNA HTG 17-MAK-2001
Homo sapiens chromosome 1 clone RP11-284F21, *** SEQUENCING IN
PROCESS ***, 14 unordered pleces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * NOTE: This is a 'working draft' sequence. It currently consists of 14 conties. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as Truns of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29757 140024: concess of 100 bp 40153 140152; gap of 100 bp 100 bp 13800 143899: gap of 100 bp 100 bp 143800 155397: contig of 11498 bp in length 165497: qap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46846 46945: contiq of 46845 bp in length
46846 46945: gap of 100 bp
46946 52507: contig of 5562 bp in length
52508 52607: gap of 100 bp
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129656: contig of 17717 bp in length
199756: gap of 100 bp
140052: contig of 10296 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: humquery@sanger.ac.uk
2062 TAAATCICTALTAAACGGCTTTGTAACCAA 2091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                      AL365181
AL365181.15 GT:13396591
HTG: HTGS_PHASE1; HTGS_DRAFT.
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155498 162028: contig of 6531 bp in length
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155498 . 162028
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/clone_lib~"RPC1-11.1"
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YRFRVALPAYPASL/IDVSLVLSELRPNDSGVYRCEVQHG I DDSSDAVEVKUVYVFLY
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LERGAQIASTGQLYAANNGGLDRCSPGWLADGSVRYPITFPSQRCCGGLDGVKTLFLF
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ESESRGAIYSIPLSEDGGGGSSTPEDPAGAFRTPLESETQSIAPPTESSEEBGVALEE
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Submitted (05-MAY-1995) U. Rauch, Max-Planck-Inst. fuer Biochemie,
Am Klopferspitz 18a, 82152 Martinsried, FRG
                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Czaniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                 Rauch, U., Forsberg, N., Kulbe, G., Arnold-Ammer, I. and Faessler, R. Cloning and sequence of mouse neurocan and brevican and their different expression during embryonic brain development Unpublished
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                                                             caaglygacillectglecogygacogggaggeagaggtgetgglygegogggggggggg
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Score 1172.2; DB 10; Length 3153; Pred. No. 4.7e-220; 0; Mismatches 348; Indels 84; Gaps

42.9%; 78.1%;

Matches 1545; Conservative

163

à q ô

Best Local Similarity

Query Match

agoctgcagcatggcccagctgttcctgcccctgctggcagccttggtcctggcccaggc 222

223 Loctgoagotttagoagatgttctggaaggagacagotcagaggacogogttttcgcgt 282

REFERENCE AUTHORS TITLE JOURNAL	FEATURES Source	SGC			×1			BASE COUNT ORIGIN	Query Matc Best Local Matches 15	149	20 GY 209 gtc	DD 96 QU	Qy 269 cgc 	Oy 329 ctc	Db 213 CTC	Qy 389 990	Db 273 GGC	QY 449 gcg	Db 333 GCG	Qy 509 tac	Db 393 TAC	Qy 569 ggt.	Db 453 GG
TGAGGCCATTGTCACAGTGACAGAAAAGCTGGAGGAACTGCAGCTGCCTCAGGAAGCGATGAGAGGGATGAGTGAATGAA	agetecactecagaagaeneagagagecectaggaegetectagaattgaaaaaea 148	atcratygtacroccacygygttctcayaayaggaaggtaaggcattggauyaagaaya 	: gaaatalgaagatgaagaagaagaggaagaagaagaagaggaggtgaggatga 1602 	99cttytygyratgyccagcgagttagcagcacgggcctgaggccttttcccac 1662 	<pre>Lgaycrageagcrcaggagaaglcatttccagggcagcaaggagagtctgcagca 1722 </pre>	tgqtgcatcaccacttcctgatggaggtcagagcttccaggcctccaagggtccatgg 1782 	accarctactgagactetgeceateccaggagaacetagcatecceatecette 184	cactc199119499caagagagutgggggaggcaactggtggtggtcgagctatctggggt - -ACTCCTGGTGGGCAACAGAAGTAGGGGGGAAACTGGGGAGCCCTGAGCTCTGGGGG		tccagccacacgggccctgaggtaccaggagctqaggcccctctqaagataattc 2016 	tygaagaactgccccagcagggacctcagtgcaggcccagcggccactgccactgacag 207		cgccagccqagytggagtggccgtggtccccqratcaggtaattctgcccaaggctc 2133 		RNU37142 3077 bp mRNA ROD	Mailus norvegicus breviran core protein mRNA, complete cds.		Rattus norvegicus	Eukaryota; Medazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;	Talcus. [Dases 1 to 3077) Yamada.H. Wattanaha K. Shimonaka M. Vinnaliki V. V.	cDNA cloning and the identification of an aggrecanase-like cleavage site in rat breview	Biochem. Biophys. Res. Commun. 216 (3), 957-963 (1995) 96074475	
Db 1266 Qy 1363 Db 1326	Qy 1423 Db 1386	Qy 1483 Ub 1446	2y 1543 Db 1506	QY 1603 Db 1551	Qy 1663 Db 1611	Qy 1723 lb 1659	QY 1783 bb 1698	Qy 1843 Db 1747	Qy 1903 Db 1806	Qy 1957 Db 1863	2017	1923	Qy 2077 Db 1983	RESULT 11	KNU3/142 LOCUS	ACCESSION VPDC:ON	KEYWORDS	ORGANISM		REFERENCE AUTHORS	TITLE	JOURNAL	

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Direct Submission
Submitted (26-SEP-1995) Yu Yamaguchi, La Jolla Cancer Research
Foundation, 10901, North Torrey Pines Road, La Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                    YRENVALPAYPASITIDVSIVLEELRPNDSGYYRCEVOUG IDDSSDAVEVKVKGVVELY
REGSARYAFSFAGAGEACAR I GAR I AT PEQLYAAY I GGYECTAAWALSDAYWYYP 1 ON
PREAZY CODMOSY POYRNYCYVGPDDLY EVOLUGEFICAAPPGKI I TWEEARDY
LERGAQ I ASTGOLY AANNGGLINCS PGWI ADGSVRYP I I I PESGACGGLIG VR KII FILE
PNQTGFPSKONRFWY CRUSAHPSAFSFASSPASOGLEA I VIYY TEKLELLU I POEAV
ESESRGAI YS I PI TEDGGGGSSTPENDA EAPRTPLESET VSVAPPTGSSEREGARIES
EPREKDIET PKEEKERERON WWYPFLSSPLPFGLET EHSLSOVSPPAGAVU GGSSS
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DCTPSEVENGGTCLREKEFERDICTPOYGGDLCDVG1HPCSPGWPAFQGGCYKHFSTR
RSWERAESQCRALGAHLTSICTPEEQDFVNDRYREYWUGINDRILBTGSRGAPL
LYENWNPGQPDSYFILSGENCVVMWHDQGQWSDVPCNYHISGTGKMGINSCGPPPQLD
LAQIFGRRAAYDTVLKYRCRIGGAQRNPLIRCGENGLWEAPQLSCVPRRPARAL
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77.8%; Pred. No. 1.2e-219;
Live 0; Mismatches 358; Indels 84; Gaps
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                                                                                                                                                                                                                                                                       /note="chondroitin sulfate proteoglycan"
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60. .2711
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2 (bases 1 to 3077)
Yamaquchi, y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brevican, a chondroitin sulfate proteoglycan of rat brain, occurs as secreted and cell surface glycosylphosphatidylinositol anchored
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Mammalia; Eutheria; Rodentia; Seluroguathi; Muridae; Hurinae;
                                                   1 (bases 1 to 2868)
Seidenberher,C.I., Richter,K., Rauch,U., Fassler,K., Garner,C.C.
and Gundelfinger,E.D.
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                                                                                                                                                                                                                               15-Nov-1995
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Submitted (27-JUN-1994) E.D. Gundelfinger, Institute for
Neurobiology Magedburg, IFN, Dept of Neurobiology & Molecular
Biology, Postfach 1860, 39008 Magdeburg, FRG
                                                                                                       X798Bl.1 Gl:509396
brevican: EGF repeal; proteodlycan; tandem repeal.
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/tissue_type="brain"
110. .2761
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/organism≂"Rattus norvegicus"
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R.norvegicus ALP mkNA for brevican.
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Gundelfinger, E.D.
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REFERENCE
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LERGAJ TASTGOLY AAWNOGLDEK SPOWLADGSVEKP IT TEPSORGGGGLEDEVATLELL
PNOTGEPSKUNKENVYCFRDSAIIPSAFSEASSPASDGLEA IVTVTEKLELLOLDOLAY
ESERSKA IYS IP IT EDAGGGSSTPEDPARAFELSETOSVAPPTGSSEEGGEALEE
ESFEKKOTETPKREKEGEN INWWPTELSSPLPTGLETEHSLEGVSPPAGAVLOVGASP
PRPRYHGFTVETTLOPPGSGSSTTSTPDGAREVGGTGSPELSGVPREREBAGSSSLED
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LY FUNNEYGOPDSYFLSGENCVVNWYHDOGONSDVEONYHLSYTCKKGLVSCGPPPQLP
LAO I FGRERLRY ANDTVLIK FORDGLIAORNLPLIRCQENGLMEAPQISCVPRRPARAL
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149 coccaqcoctgggtagoctgcagcatggcocagctgttoctgccoctgctggcagcotg 208 glocigacocagactergeagetttagragatattergaaagaagacagetraqaagae 268 ctracratecettgecaegtecaetaectgeggeraregeegageegggetgtgetg 388 ggctctcrgraggtcaagtggactttcctgtrrcggggqccgggaggcagaggtgctggtg 448 gegeggggagtgegteaaggtgaacgaggeetareggtteegegtggeactgeetgeg 508 568 628 Gaps tacccagogicgcicaccgacgiciccciygogcigagogagrigogcoccaacgacica gatatotatogotgigaggtocagoacggratogatgacagoagogacgotgiggaggto Score 1160.4; DB 10; Length 2868; Pred. No. 9.8e-218; 0; Mismatches 376; Indels 78; (Query Match
Best Local Similarity 77.2%;
Matches 1534; Conservative 98 209 146 329 389 449 509 569 ò à 9 ò q ά a QYqq ŏ q δŏ a ŏ qq

629 aaggicaaaggggicgictictciaccgagagggictcigcccgciaigcilicictit

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tctggggccraggaggcctgtgccgcattggagccaratcgccaccccqgagcagctc 748

689

qa	623	GCTGGAGCCCAGGAAGCCTGTCGCAGCGAGTCGGAATTGCCACCCCTGAGCAGCTG 68.	71
QY	749	tatgergertacet tgggggetatgageaatgtgatgetgetggetgleggateagare 808	8
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a	743	GTGAGGTACCCCATCCAGAACCCAGGAGAGCCTGTTATGGAGACATGGATGATTATGTACCT 80.	7
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Qy	1049	geetgggatggtggacetggaceetgcaggatggetagetagetggeatgtgtgtgtgtgg	0.8
1	983	GCATGGAATGGCGGCTTGGACAGATGTAGCCCTGGCTGGC	7.7
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QD	1043	TACCCCATUATICAGGGCCAGGCAACGCTGGGGGAGGCCTGCCAGGAGTCAAGACCTTC 110	0.7
Qy	1169	Il occiticocoaccagactgociteceaataayeaeageeyetieaaegietaetge 122	28
qq	1103	FECTIVITICGAACCAGACTGCTTCCCCAGCAGAACCAGTTCAAFGTCTACTGC 116	7.9
Qy	1229	ttogawartoggodoagocttotgodatrootgaggootodadoongoot coaanna 128	88
qq	1163	TTCCGAGACTCTGCCCATCCCTCTGCCTTCTCGAG	10
Qy	1289	gentetual ggaetagaggetat eg eggagi ganagagaetet ggaggaanigeaghig 134	t
QQ	1211	SCCTCTGATGGACTAGAGGCATTGTCAGAGAGAGAGAGAGA	7.0
Οy	1349	octoaggaagceacagagagagagagcatccglaggccatctactccatcccatc	0.8
QQ	1271	PETCHOLITII PETCHOGGAAGCTGTGGAAGGGAGGGGGGGGGATCTACTGGATGGCGATGAGAGAA 133	30
Qy	1409	jacggaggtggaagetenaetenagaganennageagaggeeetaggangetenta 146	9
qq	1331	SATGGGGAGGAGGAAGCTCTACCCCAGAAGACCCAGAGAGGCCCCCAGAGACTCTTCTA_139	9.0
δλ	1469	aatilgaacacaalccatygtaccgccacggggtlctcagaagaggaagtaaggca 152	8
qa	1391	AATCAGAAACCCAATCCGTTGCACCACCTACCGGGTCCTCAGAAGAGGAAGGCGAAGGC 1456	20
Οy	1529	tyqaqgaaqaaqaqaaaatatgaaqatgaaqaagagaaagaa	80
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δy	1589	agglygaggatgaggetetatgggeatggeereagegageteageageeeegggeeetgag 1648	8
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Qy	1649	cefeletececartgagecagragecaggagagagteacteteceaggecageagg 1708	80
qq	1556 (GGTTGGAAACAGAGCACTCACTCTCCCAGGTGTCCCCACCAGCCCAG 1603	3
QY	1709 9	Caglectgragectygtgrateaceetteetgatygagagteagaagetteeagget 1768	80
qq	1604	CAGTECTACAGGEGGGEGGGEGCATCACCTGCTCCCAGGCCT 1642	7
Qy		caayyylvcalyyaccacctactgayactetycccacteccayygagayaacctagca 1828	ω,
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TPREACYCDMDGFPGVRNYGLVDPDDLYDIYCYAEDLMGELFLGAPPDNVTLEEATAY
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Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis
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Ca. (bases 1 to 1519)

Jaworski, D.M., Kelly, G.M. and Hockfield, S.

BEHAB, a new member of the proteoglycan tandem repeat family of Mayluronan-binding proteins that is restricted to the brain J. Cell Biol. 125 (2), 495-509 (1994)
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21;137(2):521]]
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144674 1520 bp DNA Sequence 1 from patent US 5635370. 144674.1 GI:2469387 Unknown. Unknown. Unclassitied. Unclassitied. 1 (bases 1 to 1520) Hockfield.S. and Jaworski, D.M. DNA encoding BEHAB, a brain liyaluronar recombinant expression systems for prorecombinant expression systems for prorecombinant expressions systems for prorecombinant expressions. Location/Qualifiers 1. 1520	Lch al Sim 1080;	cercagecetygytageetgeageatggeeragetat-vetgeeeetgetygaageetet 	gtrotggocragotootgoagotttagoagatgttotggaaggagacagotcagagg 	gcgettttagcgtgcgcatagcgggcgcgccactgcagggggtgtgctcggcgg 	41 — ==	ggeteteegegggteaagtggaettteetgteeggggeegggaggeagaggtgetggt 	grgcagggagtqrqcqtcaaggtgaacgaggcctacqqqttccgcgtggcactgcctqc 	acceaqcytcyctcaccyacytctcctygcyctyaycyayctycycccaacyactc 	ggtatctatrgctgtgaggtccagoacggcatcgatgacagoaggacgctgtggaggtc 	aaggtcaaagggtcgtctttctctaccgagaaggctctgccgctatgctttctccttt 	tctggggcccaggaggctgtgccgcattggagcccacatcgccacccggagcagctc 	tatgecgectacettgggggetatgageaatgtgatgetggetggetgteggateagae 	gtgaggtatcccatccagacccacgagaggcctgttacggagacatggatgg
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